

BLAST

Basic Local Alignment Search Tool

- Your search parameters were adjusted to search for a short input sequence.

[Edit](#) [and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

Protein Sequence (8 letters)

residues 70-77 of seq id 12

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

lcl|73700

lcl|73700

Description

None

Molecule type

amino acid

Query Length

8

Database Name

nr

Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

Program

BLASTP 2.2.22+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Other reports: [Search Summary](#) [[Taxonomy reports](#)] [[Multiple alignment](#)] **NEW**

Search Parameters

Program	blastp
Word size	2
Expect value	200000
Hitlist size	100
Gapcosts	9,1
Matrix	PAM30
Threshold	11
Filter string	F
Genetic Code	1
Window Size	40

Database

Posted date	Jan 3, 2010 5:44 PM
Number of letters	3,505,793,397
Number of sequences	10,274,250
Entrez query	none

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.36992	0.294
K	0.287801	0.11
H	1.64552	0.61

Results Statistics

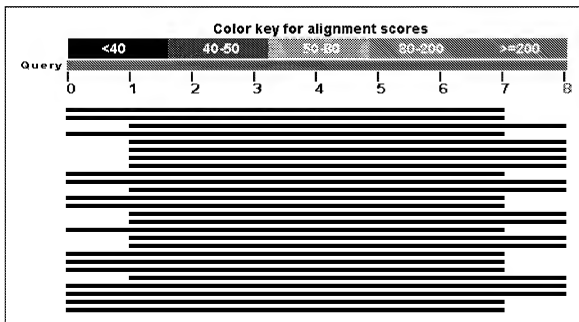
Length adjustment	0
Effective length of query	8
Effective length of database	3505793397
Effective search space	28046347176
Effective search space used	28046347176

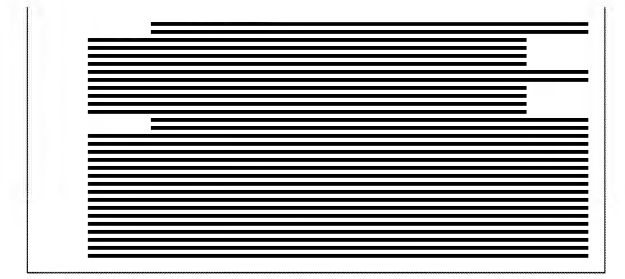
[Graphic Summary](#)[Show Conserved Domains](#)

No putative conserved domains have been detected

**Distribution of 122 Blast Hits on the Query Sequence**

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.





Descriptions

E	Sequences producing significant alignments:	Score	
		(Bits)	Value
gmb CEA27849.1	thioredoxin reductase [uncultured archaeon]	23.1	3077
gb ACF73045.1	putative NADPH-dependent FMN reductase [Halomo...	23.1	3077
ref XP_05745499.1	amino acid permease [Corynebacterium effec...	23.1	3077
gb EED39512.1	hypothetical protein NECHADRAFT_70309 [Nectria...	23.1	3077
ref XP_04782353.1	NCS2 family nucleobase:cation symporter-2 ...	23.1	3077
gb EEL18878.1	hypothetical protein Pmar_PMAR006502 [Perkinsu...	23.1	3077
gb EEL13661.1	hypothetical protein Pmar_PMAR016316 [Perkinsu...	23.1	3077
ref XP_001715648.2	PREDICTED: hypothetical protein [Homo sap...]	23.1	3077
ref XP_003327263.1	glycosyl transferase, family 2 [Xylanimon...	23.1	3077
ref XP_002504543.1	predicted protein [Micromonas sp. RCC299]...	23.1	3077
ref XP_002522795.1	conserved hypothetical protein [Ricinus C...	23.1	3077
ref XP_002490603.1	NAD dependent epimerase/dehydratase, puta...	23.1	3077
ref XP_002601066.1	hypothetical protein BRAFLDRAFT_75502 [Br...	23.1	3077
ref XP_001354725.2	GA10819 [Drosophila pseudoobscura pseudoo...	23.1	3077
ref XP_002061592.1	GK20941 [Drosophila willistonii] >gb EDW72...	23.1	3077
ref XP_002046966.1	GJ12254 [Drosophila virilis] >gb EDW69208...	23.1	3077
ref XP_002623356.1	GL20243 [Drosophila persimilis] >gb EDW27...	23.1	3077
gb EDP30649.1	vacuolar targeting protein Atg24, putative [As...	23.1	3077
ref XP_001847639.1	zinc finger protein [Culex quinquefasciat...	23.1	3077
ref XP_001756481.1	predicted protein [Physcomitrella patens ...]	23.1	3077
gb A6W82164.1	spouty 2 [Pantherophis guttatus]	23.1	3077
ref XP_018965905.1	putative glutamate-ammonia-ligase adenylyl...	23.1	3077
ref XP_001475732.1	PREDICTED: hypothetical protein [Mus musc...	23.1	3077
ref XP_064271.2	PREDICTED: hypothetical protein [Mus musculu...	23.1	3077
ref XP_001819060.1	predicted protein [Magnaporthe grisea 70-...	23.1	3077
ref XP_001310397.1	hypothetical protein [Trichomonas vaginal...	23.1	3077
ref XP_046098.1	hypothetical protein AAur_0278 [Arthrobacter...	23.1	3077
ref XP_001466749.1	vacuolar targeting protein Atg24, putativ...	23.1	3077
ref YP_029499.1	NADH dehydrogenase subunit 5 [Apus apus] >em...	23.1	3077
ref NP_148224.2	hypothetical protein APE_2029.1 [Aeropyrum p...	23.1	3077
ref XP_001796668.1	hypothetical protein SNOG_06291 [Phaeosph...	23.1	3077
ref XP_001054071.1	PREDICTED: hypothetical protein [Rattus n...	23.1	3077
ref NP_824938.1	hypothetical protein SAV_3761 [Streptomyces ...]	23.1	3077
gb AAD13661.1	surface antigen [Hepatitis B virus]	23.1	3077
ref YP_261572.1	negative regulator of flagellin synthesis Fl...	23.1	3077
ref NP_001034904.1	adenosine A2a receptor a [Danio rerio] >g...	23.1	3077
ref NP_003667.1	ACR265Cp [Ashbya gossypii ATCC 10895] >gb AA...	23.1	3077
ref NP_008256.1	phage-related putative exported protein [Bor...	23.1	3077
ref NP_037321.1	putative amino-acid permease [Corynebacteriu...	23.1	3077
ref XP_751524.1	vacuolar targeting protein Atg24 [Aspergillu...	23.1	3077
ref XP_000066442.1	conserved hypothetical protein [Streptomyce...	22.7	4129
ref XP_048727.1	hypothetical protein MGG_00517 [Magnaporthe ...]	22.7	4129
ref GP_04120432.1	AMP-dependent synthetase and ligase [Caulo...	22.3	5541
gmb C5875373.1	putative secreted phytase [Streptomyces scabi...	22.3	5541
ref GP_05237507.1	long-chain-fatty-acid--CoA ligase [Mycobac...	22.3	5541
ref GP_05234857.1	acyl-CoA synthetase [Mycobacterium intrace...	22.2	5541
ref GP_04747235.1	acyl-CoA synthetase [Mycobacterium kansas...	22.3	5541

ref YP_04603923.1	hypothetical protein MCAG_00186 [Micromono...	22.3	5541
gb EHW03467.1	predicted protein [Ajellomyces capsulatus G186AR]	22.3	5541
ref YP_002516596.1	acyl-CoA synthetase [Caulobacter crescent...	22.3	5541
ref YP_05015365.1	two-component system sensor kinase [Strept...	22.3	5541
ref YP_050170168.1	putative fatty-acid--CoA ligase FadD [Myc...	22.3	5541
emb CQ77362.1	FadD28 protein [Mycobacterium chelonae]	22.3	5541
ref YP_027009.1	acyl-CoA synthase [Mycobacterium smegmatis s...	22.3	5541
ref XP_027951.1	acyl-CoA synthetase [Mycobacterium avium 104...	22.3	5541
ref NP_059153.1	acyl-CoA synthetase [Mycobacterium avium sub...	22.3	5541
ref NP_019981.1	acyl-CoA synthetase [Caulobacter crescentus ...]	22.3	5541
ref YP_001510807.1	DNA polymerase III subunits gamma and tau...	21.8	5541
gb ACT90703.1	large S protein [Hepatitis B virus]	21.8	7434
gb ACT90699.1	S protein [Hepatitis B virus]	21.8	7434
gb AA56324.1	profilaggrin [Homo sapiens]	21.8	7434
gb AA35467.1	profilaggrin [Homo sapiens]	21.8	7434
ref NP_002607.1	filaggrin [Homo sapiens] >sp P20930.3 FILA_H...	21.8	7434
ref YP_001598694.1	integrase catalytic region [Frankia sp. E...]	21.8	7434
ref YP_04927765.1	fibronectin type III domain containing pro...	21.4	9975
emb CAL54905.1	unnamed protein product [Ostreococcus tauri]	21.4	9975
gb AAC18046.1	FIP2 [Homo sapiens] >gb AAG00497.1 FIP2 [Homo...	21.4	9975
gb AAC18047.1	FIP2 [Homo sapiens]	21.4	9975
gb AAA25751.1	2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydr...	21.4	9975
ref YP_01039628.1	hypothetical protein NAP1_04965 [Erythroba...	21.4	9975
ref YP_003313354.1	FHA domain-containing protein [Sanguibact...	21.0	13384
ref YP_003098106.1	DNA topoisomerase I [Actinosynnema mirum ...]	21.0	13384
ref XP_002956267.1	flagellin [Desulfovibrio magneticus RS-1]...	21.0	13384
ref YP_04634430.1	Large exoprotein involved in heme utilizat...	21.0	13384
ref XP_002364099.1	Pc22g00530 [Penicillium chrysogenum Wisco...	21.0	13384
ref NP_001129936.1	Small family member (sma-9) [Caenorhabdit...	21.0	13384
ref NP_001129935.1	Small family member (sma-9) [Caenorhabdit...	21.0	13384
ref XP_001269098.1	conserved hypothetical protein [Aspergill...	21.0	13384
gb AA2862.1	zinc finger transcription factor SMA-9 [Caenor...	21.0	13384
gb AA2862.1	zinc finger transcription factor SMA-9 [Caenor...	21.0	13384
gb AA54949.1	SMA-9 class B [Caenorhabditis elegans]	21.0	13384
ref XP_296615.2	PREDICTED: similar to CG9066-PA [Apis mellif...	21.0	13384
ref NP_001024879.1	Small family member (sma-9) [Caenorhabdit...	21.0	13384
ref NP_001024881.1	Small family member (sma-9) [Caenorhabdit...	21.0	13384
ref NP_741897.2	Small family member (sma-9) [Caenorhabditis ...]	21.0	13384
ref NP_001024884.1	Small family member (sma-9) [Caenorhabdit...	21.0	13384
ref NP_001024880.1	Small family member (sma-9) [Caenorhabdit...	21.0	13384
ref NP_001024878.1	Small family member (sma-9) [Caenorhabdit...	21.0	13384
ref NP_001024883.1	Small family member (sma-9) [Caenorhabdit...	21.0	13384
ref NP_001024877.1	Small family member (sma-9) [Caenorhabdit...	21.0	13384
ref NP_741896.2	Small family member (sma-9) [Caenorhabditis ...]	21.0	13384
ref XP_002644111.1	C. briggsae CBR-SMA-9 protein [Caenorhabd...	21.0	13384
ref YP_0505978.1	tannase and feruloyl esterase [Ralstonia met...	20.6	13384
gb EFA2206.1	hypothetical protein PANDA_008701 [Ailuropora ...]	20.6	17959
gb EFA8966.1	conserved domain protein [Staphylococcus epide...	20.6	17959
ref YP_06217945.1	YD repeat protein [Acidovorax avenae subsp...	20.6	17959
gb EFA09862.1	hypothetical protein TcasGA2_TC012010 [Triboli...	20.6	17959
ref NP_001361595.1	nanos-like protein [Saccoglossus kowalevs...	20.6	17959
ref YP_05970998.1	adhesin [Acinetobacter lwoffii SH145] >gb ...	20.6	17959

[gi|55561921.1](#) conserved hypothetical protein [Phytophthora i... [20.6](#) 17959

Alignments [Select All](#) [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#) [NEW](#)

>**emb|CBH37829.1**| thioredoxin reductase [uncultured archaeon]
Length=312

Score = 23.1 bits (47), Expect = 3077
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 GSTRTST 7
Sbjct 265 GSTRTST 271

>**gb|ACF77045.1**| putative NADPH-dependent FMN reductase [Halomonas sp. HAL1]
Length=221

Score = 23.1 bits (47), Expect = 3077
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 GSTRTST 7
Sbjct 9 GSTRTST 15

>**ref|ZP_05749499.1**| amino acid permease [Corynebacterium efficiens YS-314]
gb|EEW50349.1| amino acid permease [Corynebacterium efficiens YS-314]
Length=568

Score = 23.1 bits (47), Expect = 3077
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 SIRTSTG 8
Sbjct 543 SIRTSTG 549

Score = 17.2 bits (33), Expect = 188688
Identities = 5/6 (83%), Positives = 5/6 (83%), Gaps = 0/6 (0%)

Query 2 SIRTST 7
Sbjct 539 SIRTST 544

>**gb|EEU39512.1**| hypothetical protein NECHADRAFT_70309 [Nectria haematococca mpVI
77-13-4]
Length=483

Score = 23.1 bits (47), Expect = 3077
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 GSTRTST 7
Sbjct 278 GSTRTST 284

>**ref|ZP_04783253.1**| NCS2 family nucleobase:cation symporter-2 [Weissella parames
ATCC 33313]
gb|EER74751.1| NCS2 family nucleobase:cation symporter-2 [Weissella paramesente
ATCC 33313]
Length=434

Score = 23.1 bits (47), Expect = 3077
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 STRTSTG 8
Sbjct 4 STRTSTG 10

>**gb|EER18878.1**| hypothetical protein Pmar_PMAR006502 [Perkinsus marinus ATCC
50983]
Length=50

Score = 23.1 bits (47), Expect = 3077
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 STRTSTG 8
Sbjct 22 STRTSTG 28

>**gb|EER13661.1|** hypothetical protein Pmar_PMAR016316 [Perkinsus marinus ATCC 50983]
Length=548

Score = 23.1 bits (47), Expect = 3077
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 STRTSTG 8
Sbjct 19 STRTSTG 25

>**ref|XP_001715648.2|** **G** PREDICTED: hypothetical protein [Homo sapiens]
Length=93

GENE ID: 100134320 LOC100134320 | hypothetical protein LOC100134320 [Homo sapiens]

Score = 23.1 bits (47), Expect = 3077
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 STRTSTG 8
Sbjct 18 STRTSTG 24

Score = 23.1 bits (47), Expect = 3077
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 STRTSTG 8
Sbjct 28 STRTSTG 34

>**ref|YP_003327263.1|** glycosyl transferase, family 2 [Xylanimonas cellulosilytica 15894]
gb|ACZ31705.1| glycosyl transferase, family 2 [Xylanimonas cellulosilytica DSM 15894]
Length=306

Score = 23.1 bits (47), Expect = 3077
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 GSTRTST 7
Sbjct 293 GSTRTST 299

>**ref|XP_002504543.1|** **G** predicted protein [Micromonas sp. RCC299]
gb|ACO65801.1| **G** predicted protein [Micromonas sp. RCC299]
Length=559

GENE ID: 8246104 MICPUN_50521 | hypothetical protein [Micromonas sp. RCC299]

Score = 23.1 bits (47), Expect = 3077
Identities = 7/8 (87%), Positives = 8/8 (100%), Gaps = 0/8 (0%)

Query 1 GSTRTSTG 8
Sbjct 83 GTTSTSTG 90

>**ref|XP_002523795.1|** **G** conserved hypothetical protein [Ricinus communis]
gb|EEF38521.1| conserved hypothetical protein [Ricinus communis]
Length=1237

GENE ID: 8271907 RCOM_1280790 | hypothetical protein [Ricinus communis]

Score = 23.1 bits (47), Expect = 3077

Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 STRTSTG 8
STRTSTG
Sbjct 440 STRTSTG 446

>ref|XP_002480603.1| **G** NAD dependent epimerase/dehydratase, putative [Talaromyces ATCC 10500]

gb|EED20169.1| **G** NAD dependent epimerase/dehydratase, putative [Talaromyces sti ATCC 10500]
Length=356

GENE ID: 8097825 TSTA_034080 | NAD dependent epimerase/dehydratase, putative [Talaromyces stipitatus ATCC 10500]

Score = 23.1 bits (47), Expect = 3077
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 GSTRTST 7
GSTRTST
Sbjct 234 GSTRTST 240

>ref|XP_002601066.1| **G** hypothetical protein BRAFLDRAFT_75502 [Branchiostoma flor
gb|EEN57078.1| **G** hypothetical protein BRAFLDRAFT_75502 [Branchiostoma floridae]
Length=2283

GENE ID: 7235864 BRAFLDRAFT_75502 | hypothetical protein [Branchiostoma floridae] (10 or fewer PubMed links)

Score = 23.1 bits (47), Expect = 3077
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 GSTRTST 7
GSTRTST
Sbjct 2266 GSTRTST 2272

Score = 18.0 bits (35), Expect = 104804
Identities = 5/5 (100%), Positives = 5/5 (100%), Gaps = 0/5 (0%)

Query 3 TRTST 7
TRTST
Sbjct 2204 TRTST 2208

>ref|XP_001354725.2| **G** GA10819 [Drosophila pseudoobscura pseudoobscura]
gb|EAL31780.2| GA10819 [Drosophila pseudoobscura pseudoobscura]
Length=728

GENE ID: 4815191 Dpse|GA10819 | GA10819 gene product from transcript GA10819-RA [Drosophila pseudoobscura pseudoobscura] (10 or fewer PubMed links)

Score = 23.1 bits (47), Expect = 3077
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 STRTSTG 8
STRTSTG
Sbjct 651 STRTSTG 657

>ref|XP_002061502.1| **G** GK20941 [Drosophila willistonii]
gb|EDW72488.1| **G** GK20941 [Drosophila willistonii]
Length=444

GENE ID: 6638486 Dwil|GK20941 | GK20941 gene product from transcript GK20941-RA [Drosophila willistonii] (10 or fewer PubMed links)

Score = 23.1 bits (47), Expect = 3077
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 STRTSTG 8
STRTSTG
Sbjct 251 STRTSTG 257